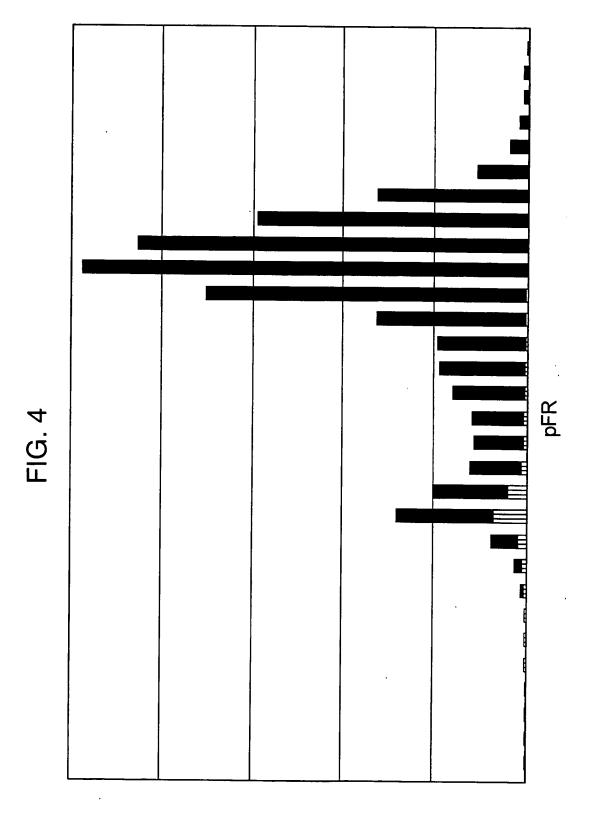
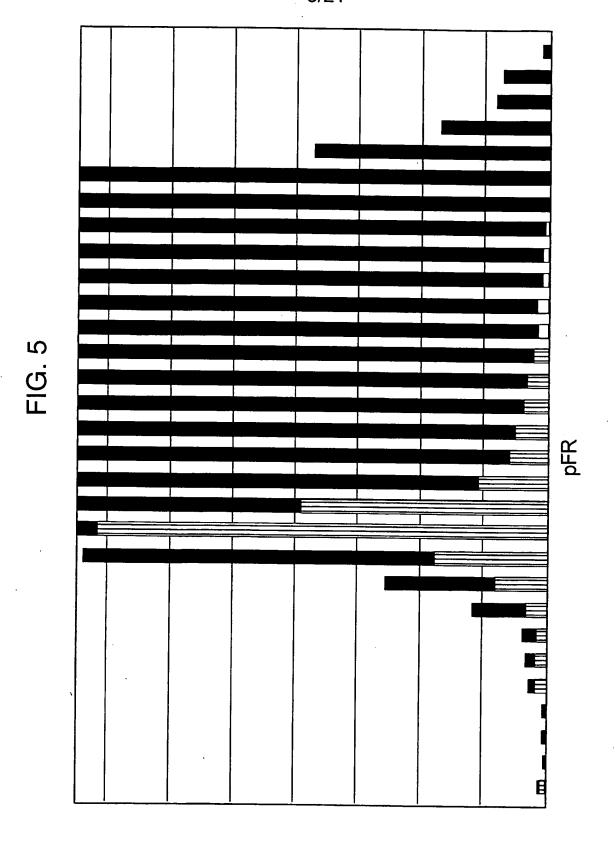
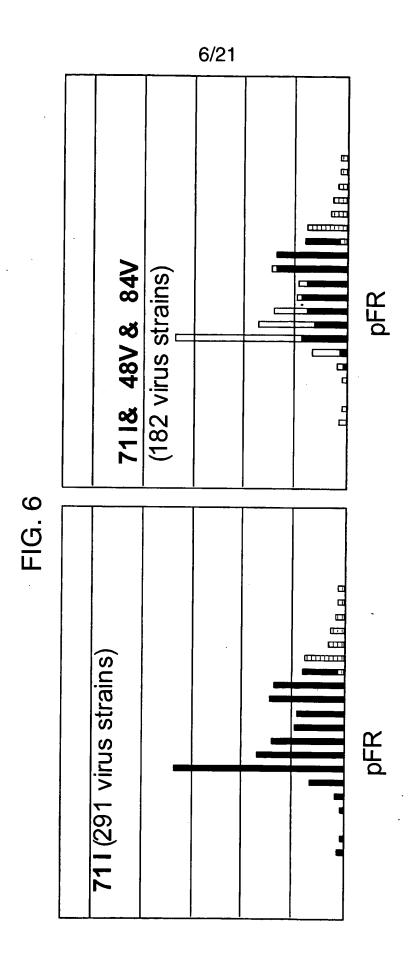
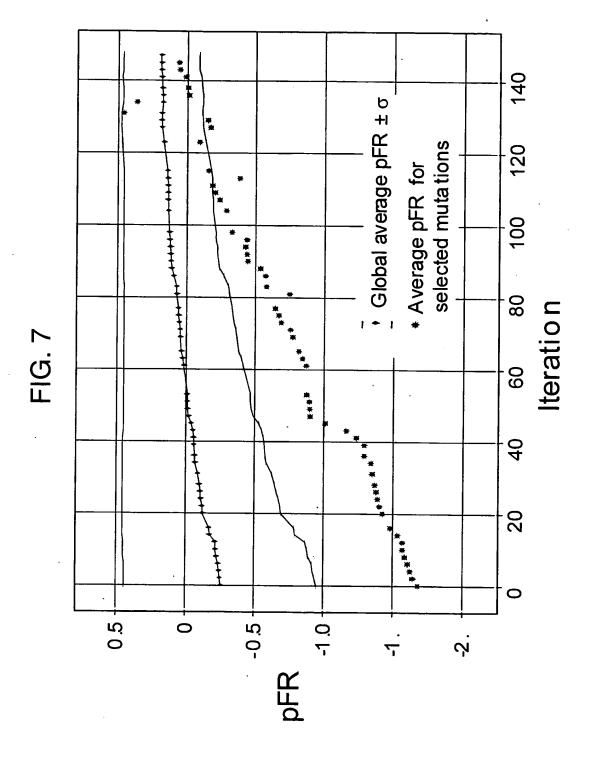


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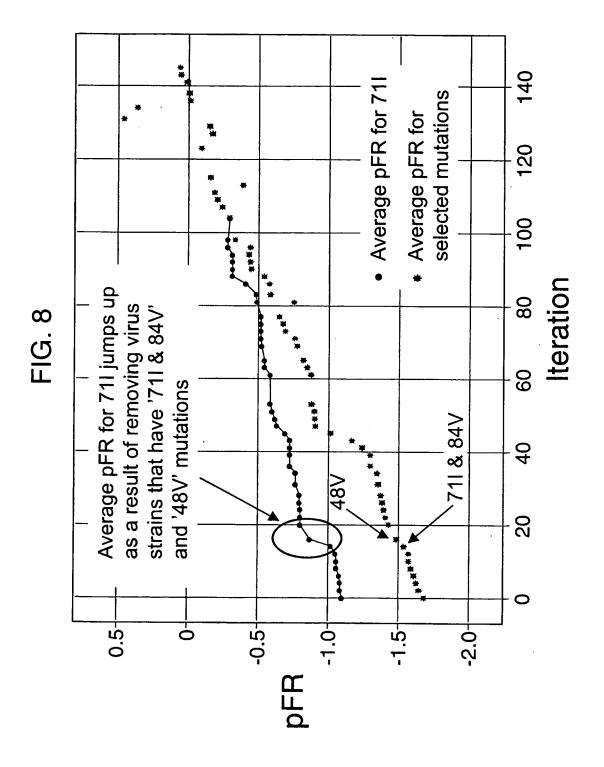
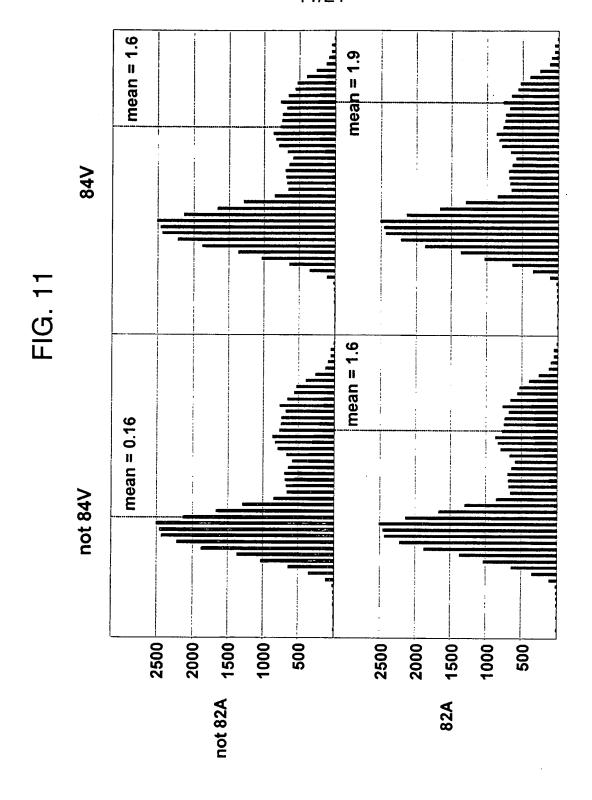


FIG. 9

Commission											<u>a</u>	Position	ign									
	က	10 12 15 19	12	15	19	8	24	30	32	36	37	41.	791	8	なな	26	3 7	1 7	<b>4</b> 75	11	20 24 30 32 36 37 41 46 48 54 62 63 71 74 75 77 82 84 93	4 93
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\$											Z		$\underline{\underline{\mathbb{N}}}$		<u>≥</u>	ш	<i>&gt;</i>				≥	>

FIG. 10

Vinssampe Vinssampe Vinssampe	1	· -	_ ,	<del></del>		-0.14 0.22 -0.17	960
gession model log/FO shift	230 (660) (090)				0.67/	Other interactions	predicted log(PC)



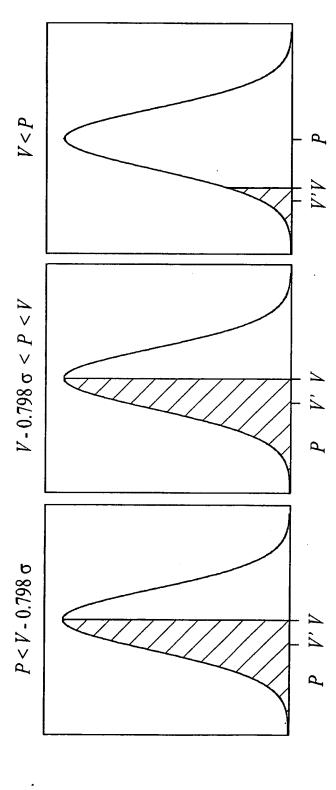


FIG. 12

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Mutation	log(FC) shift	Prevalence in dataset
74	05:0	1,027
NOS	-0.39	1,715
<b>54</b>	1.33	35
735	0.45	357
<b>35</b>	0.38	2,224
731	0.53	<del>69</del> 2
MZ8	99:0	8
84 44	1.73	2
84C	62.0	<i>L</i> 9

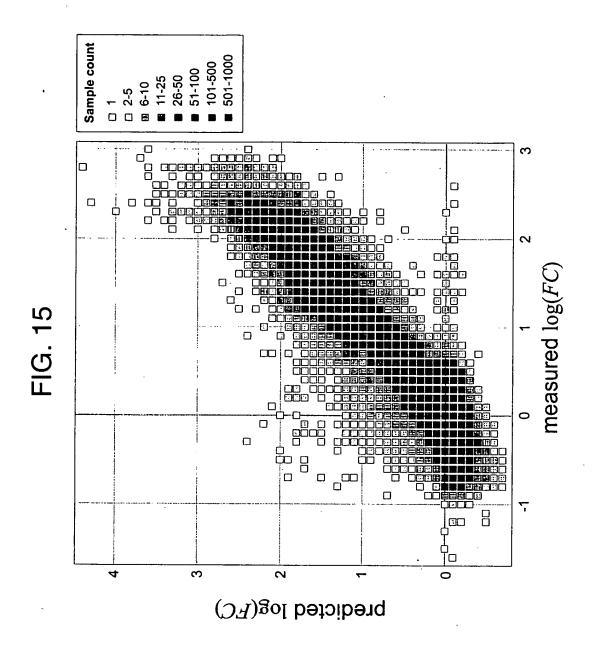


FIG 16

pecificity	89.7%	94.4%	954%
Sensitivity S	89.8%	35.3%	<b>380%</b>
Leave-one-out prediction error	10.2%	64%	26%
esistant fraction (FC>3.5)	50.1%	50.1%	38.3%
Nr. of F samples	<del>8</del>	<del>6</del>	34,502
	<b>Decision tree</b>	Linear model	Linear model

Regression model identifies 53 single mutations and 96 pairs of mutations as having a positive or negative contribution to RTV susceptibility 20 out of 22 mutations from IAS list<sup>(1)</sup> are confirmed to be significant by regression model

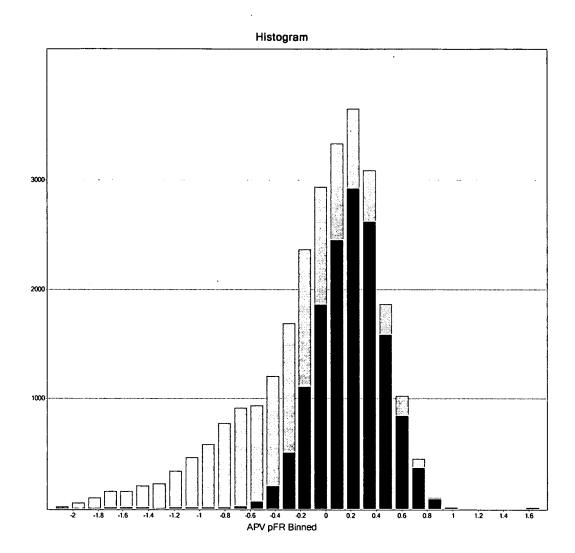


FIG. 17

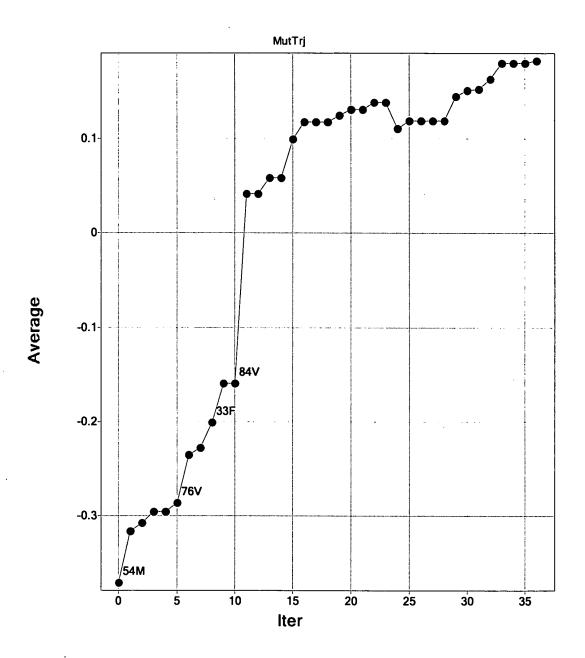


FIG. 18

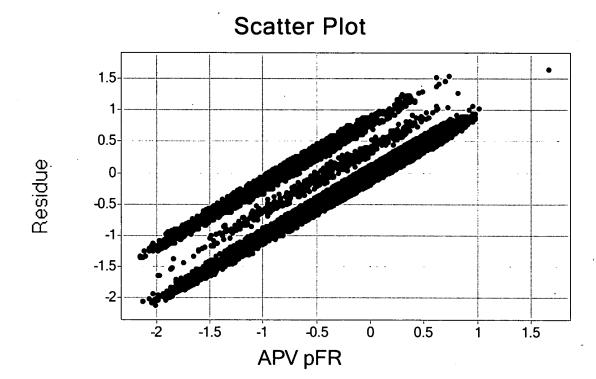


FIG. 19

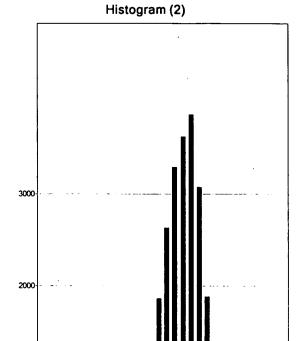


FIG. 20

-1 -0.8-.. -... -0.2 0 0.2 0.4 0.6 0.8 1 1.2 1.4 1.6 Residue Binned

1000

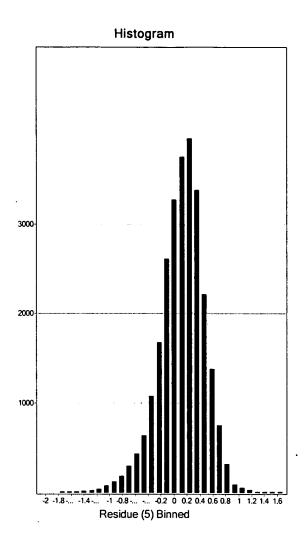


FIG. 21